



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/937,908A

DATE: 09/15/2004

TIME: 11:07:04

Input Set : A:\213721.ST25.txt

Output Set: N:\CRF4\09152004\I937908A.raw

3 <110> APPLICANT: Feussner et al.  
 5 <120> TITLE OF INVENTION: Linoleate- and Linolenate-Lipoxygenase-Mutants  
 7 <130> FILE REFERENCE: 213721  
 9 <140> CURRENT APPLICATION NUMBER: US 09/937,908A  
 10 <141> CURRENT FILING DATE: 2002-01-07  
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP00/02545  
 13 <151> PRIOR FILING DATE: 2000-03-22  
 15 <150> PRIOR APPLICATION NUMBER: DE 19914464.8  
 16 <151> PRIOR FILING DATE: 1999-03-30  
 18 <160> NUMBER OF SEQ ID NOS: 5  
 20 <170> SOFTWARE: PatentIn Ver. 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 878  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Cucumis sativus  
 27 <400> SEQUENCE: 1  
 28 Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr  
 29 1 5 10 15  
 31 Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp  
 32 20 25 30  
 34 Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu  
 35 35 40 45  
 37 Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu  
 38 50 55 60  
 40 Asp Asn Phe Thr Glu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile  
 41 65 70 75 80  
 43 Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys  
 44 85 90 95  
 46 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly  
 47 100 105 110  
 49 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe  
 50 115 120 125  
 52 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu  
 53 130 135 140  
 55 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe  
 56 145 150 155 160  
 58 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg  
 59 165 170 175  
 61 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro  
 62 180 185 190  
 64 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly  
 65 195 200 205  
 67 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr

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68      210      215      220
70 Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
71 225      230      235      240
73 Gly Thr Thr Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro
74      245      250      255
76 Arg Ser Arg Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met
77      260      265      270
79 Ser Leu Asp Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys
80      275      280      285
82 Met Ser Asp Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile
83      290      295      300
85 Lys Pro Gly Leu Gln Ser Ile Phe Asp Val Thr Pro Asn Glu Phe Asp
86 305      310      315      320
88 Asn Phe Lys Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro
89      325      330      335
91 Phe Asn Ala Phe Lys Thr Leu Thr Glu Asp Leu Thr Pro Pro Leu Phe
92      340      345      350
94 Lys Ala Leu Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr
95      355      360      365
97 Pro Glu Val Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu
98      370      375      380
100 Phe Ala Arg Glu Met Leu Ala Gly Pro Asn Pro Leu Leu Ile Arg Arg
101 385      390      395      400
103 Leu Glu Ala Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly
104      405      410      415
106 Asn Gln Asn Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp
107      420      425      430
109 Gly Leu Thr Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val
110      435      440      445
112 Asp Phe His Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr
113      450      455      460
115 Ser Thr Lys Thr Tyr Ala Thr Arg Thr Leu Leu Leu Lys Asp Asp
116 465      470      475      480
118 Gly Thr Leu Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln
119      485      490      495
121 Gly Asp Gln Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn
122      500      505      510
124 Gly Val Gln Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val
125      515      520      525
127 Asn Asp Val Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His
128      530      535      540
130 Ala Val Leu Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val
131 545      550      555      560
133 Leu His Pro Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met
134      565      570      575
136 Phe Ile Asn Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu
137      580      585      590
139 Ile Glu Thr Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser
140      595      600      605

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142 Ile Leu Tyr Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn
143      610                      615                      620
145 Leu Met Lys Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly
146 625                      630                      635                      640
148 Leu Arg Leu Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp
149                      645                      650                      655
151 Ile Trp Ser Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr
152                      660                      665                      670
154 Tyr Lys Asp Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp
155                      675                      680                      685
157 Trp Asn Glu Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro
158      690                      695                      700
160 Trp Trp Pro Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr
161 705                      710                      715                      720
163 Thr Ile Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly
164                      725                      730                      735
166 Gln Tyr Pro Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg
167      740                      745                      750
169 Arg Phe Met Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser
170      755                      760                      765
172 Asn Pro Glu Lys Ala Phe Leu Arg Thr Ile Cys Ser Glu Leu Gln Ala
173      770                      775                      780
175 Leu Val Ser Ile Ser Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp
176 785                      790                      795                      800
178 Glu Val Tyr Leu Gly Gln Arg Ala Ser Ile Asp Trp Thr Ser Asp Lys
179                      805                      810                      815
181 Ile Ala Leu Glu Ala Phe Glu Lys Phe Gly Lys Asn Leu Phe Glu Val
182                      820                      825                      830
184 Glu Asn Arg Ile Met Glu Arg Asn Lys Glu Val Asn Leu Lys Asn Arg
185                      835                      840                      845
187 Ser Gly Pro Val Asn Leu Pro Tyr Thr Leu Leu Val Pro Ser Ser Asn
188      850                      855                      860
190 Glu Gly Leu Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
191 865                      870                      875

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194 &lt;210&gt; SEQ ID NO: 2

195 &lt;211&gt; LENGTH: 10

196 &lt;212&gt; TYPE: PRT

197 &lt;213&gt; ORGANISM: Artificial

199 &lt;220&gt; FEATURE:

200 &lt;223&gt; OTHER INFORMATION: Synthetic

202 &lt;400&gt; SEQUENCE: 2

204 Thr Val Asn Asp Val Gly Tyr His Gln Leu

205 1 5 10

208 &lt;210&gt; SEQ ID NO: 3

209 &lt;211&gt; LENGTH: 10

210 &lt;212&gt; TYPE: PRT

211 &lt;213&gt; ORGANISM: Artificial

213 &lt;220&gt; FEATURE:

214 &lt;223&gt; OTHER INFORMATION: Synthetic

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216 <400> SEQUENCE: 3  
218 Ile Glu Thr Thr His Tyr Pro Ser Lys Tyr  
219 1 5 10  
221 <210> SEQ ID NO: 4  
222 <211> LENGTH: 59  
223 <212> TYPE: DNA  
224 <213> ORGANISM: Artificial  
226 <220> FEATURE:  
227 <223> OTHER INFORMATION: Oligonucleotide primer  
230 <400> SEQUENCE: 4  
231 gcttatgtaa ctgttaatga ttctcggttac catcaactta ttagtcattg gttgcatac 59  
233 <210> SEQ ID NO: 5  
234 <211> LENGTH: 57  
235 <212> TYPE: DNA  
236 <213> ORGANISM: Artificial  
238 <220> FEATURE:  
239 <223> OTHER INFORMATION: Oligonucleotide primer  
242 <400> SEQUENCE: 5  
243 gtatgcaacc aatgactaat aagttgatgg taaccgaaat cattaacagt tacataa 57

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/15/2004  
PATENT APPLICATION: US/09/937,908A      TIME: 11:07:05

Input Set : A:\213721.ST25.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5

**VERIFICATION SUMMARY**

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